

SEQUENCE LISTING

<110> Baum, Peter Robert
 Fanslow III, William C.
 <120> Molecules Designated LDCAM
 <130> 2873-US
 <140> to be assigned--
 <141> 2001-02-06
 <140> PCT/US99/17905
 <141> 1999-08-05
 <150> 60/095,672
 <151> 1998-08-07
 <160> 10
 <170> PatentIn Ver. 2.0

<210> 1
 <211> 1535
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> 16..1341

<400> 1

gcggccgcgc ccgac atg gcg agt gta gtg ctg ccg agc gga tcc cag tgt 51
 Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys
 1 5 10

gcg gca gca gca gca gca gca gct ccc ggg ctc cgg ctc cgg ctt 99
 Ala Ala Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu
 15 20 25

ctg ctg ttg ctc ttc tcc gcc gca ctg atc ccc aca ggt gat ggg 147
 Leu Leu Leu Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly
 30 35 40

cag aat ctg ttt acg aaa gac gtg aca gtg atc gag gga gag gtt gcg 195
 Gln Asn Leu Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala
 45 50 55 60

acc atc agt tgc caa gtc aat aag agt gac gac tct gtg att cag cta 243
 Thr Ile Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu
 65 70 75

ctg aat ccc aac agg cag acc att tat ttc agg gac ttc agg cct ttg 291
 Leu Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
 80 85 90

aag gac agc agg ttt cag ttg ctg aat ttt tct agc agt gaa ctc aaa 339
 Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys
 95 100 105

gta tca ttg aca aac gtc tca att tct gat gaa gga aga tac ttt tgc 387
 Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys
 110 115 120

cag ctc tat acc gat ccc cca cag gaa agt tac acc acc atc aca gtc Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val 125 130 135 140	435
ctg gtc cca cca cgt aat ctg atg atc gat atc cag aaa gac act gcg Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala 145 150 155	483
gtg gaa ggt gag gag att gaa gtc aac tgc act gct atg gcc agc aag Val Glu Gly Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys 160 165 170	531
cca gcc acg act atc agg tgg ttc aaa ggg aac aca gag cta aaa ggc Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly 175 180 185	579
aaa tcg gag gtg gaa gag tgg tca gac atg tac act gtg acc agt cag Lys Ser Glu Val Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln 190 195 200	627
ctg atg ctg aag gtg cac aag gag gac gat ggg gtc cca gtg atc tgc Leu Met Leu Lys Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys 205 210 215 220	675
cag gtg gag cac cct gcg gtc act gga aac ctg cag acc cag cggttat Gln Val Glu His Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr 225 230 235	723
cta gaa gta cag tat aag cct caa gtg cac att cag atg act tat cct Leu Glu Val Gln Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro 240 245 250	771
cta caa ggc tta acc cgg gaa ggg gac gcg ctt gag tta aca tgt gaa Leu Gln Gly Leu Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu 255 260 265	819
gcc atc ggg aag ccc cag cct gtg atg gta act tgg gtg aga gtc gat Ala Ile Gly Lys Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp 270 275 280	867
gat gaa atg cct caa cac gcc gta ctg tct ggg ccc aac ctg ttc atc Asp Glu Met Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile 285 290 295 300	915
aat aac cta aac aaa aca gat aat ggt aca tac cgc tgt gaa gct tca Asn Asn Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser 305 310 315	963
aac ata gtg ggg aaa gct cac tcg gat tat atg ctg tat gta tac gat Asn Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp 320 325 330	1011
ccc ccc aca act atc cct cct ccc aca aca acc acc acc acc acc acc Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr 335 340 345	1059
acc acc acc acc acc atc ctt acc atc atc aca gat tcc cga gca ggt Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly 350 355 360	1107
gaa gaa ggc tcg atc agg gca gtg gat cat gcc gtg atc ggt ggc gtc Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val 365 370 375 380	1155
gtg ccg gtg gtg ttc gcc atg ctg tgc ttg ctc atc att ctg ggg Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly 385 390 395	1203

cgc tat ttt gcc aga cat aaa ggt aca tac ttc act cat gaa gcc aaa	1251																												
Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys																													
400	405		410	gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa	1299	Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu		415	420		425	gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc	1341	Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile		430	435		440	tagatcagcc tttttgttgc aatgagggtgt ccaactggcc ctattnagat gataaaagaga	1401	cagtgtatatt ggaacttgcg agaaaattcgt gtgtttttt atgaatgggt ggaaagggtgt	1461	gagactggga aggcttggga tttgctgtgt aaaaaaaaaaaa aaaaaaatgtt ctttggaaag	1521	aaaaaaaaagcgg ccgcctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc	1581	atacatgcta tttccat	1598
	410																												
gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa	1299																												
Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu																													
415	420		425	gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc	1341	Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile		430	435		440	tagatcagcc tttttgttgc aatgagggtgt ccaactggcc ctattnagat gataaaagaga	1401	cagtgtatatt ggaacttgcg agaaaattcgt gtgtttttt atgaatgggt ggaaagggtgt	1461	gagactggga aggcttggga tttgctgtgt aaaaaaaaaaaa aaaaaaatgtt ctttggaaag	1521	aaaaaaaaagcgg ccgcctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc	1581	atacatgcta tttccat	1598								
	425																												
gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc	1341																												
Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile																													
430	435		440	tagatcagcc tttttgttgc aatgagggtgt ccaactggcc ctattnagat gataaaagaga	1401	cagtgtatatt ggaacttgcg agaaaattcgt gtgtttttt atgaatgggt ggaaagggtgt	1461	gagactggga aggcttggga tttgctgtgt aaaaaaaaaaaa aaaaaaatgtt ctttggaaag	1521	aaaaaaaaagcgg ccgcctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc	1581	atacatgcta tttccat	1598																
	440																												
tagatcagcc tttttgttgc aatgagggtgt ccaactggcc ctattnagat gataaaagaga	1401																												
cagtgtatatt ggaacttgcg agaaaattcgt gtgtttttt atgaatgggt ggaaagggtgt	1461																												
gagactggga aggcttggga tttgctgtgt aaaaaaaaaaaa aaaaaaatgtt ctttggaaag	1521																												
aaaaaaaaagcgg ccgcctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc	1581																												
atacatgcta tttccat	1598																												

<210> 2
<211> 442
<212> PRT
<213> Homo sapien

<400> 2

Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala																																																																											
1	5		10		15	Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu		20	25		30	Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe		35	40		45	Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys		50	55		60	Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn		65	70		75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190
	10		15	Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu		20	25		30	Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe		35	40		45	Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys		50	55		60	Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn		65	70		75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190		
	15																																																																										
Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu																																																																											
20	25		30	Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe		35	40		45	Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys		50	55		60	Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn		65	70		75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190								
	30																																																																										
Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe																																																																											
35	40		45	Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys		50	55		60	Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn		65	70		75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190														
	45																																																																										
Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys																																																																											
50	55		60	Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn		65	70		75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																				
	60																																																																										
Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn																																																																											
65	70		75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																										
	75		80	Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg		85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																												
	80																																																																										
Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg																																																																											
85	90		95	Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr		100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																		
	95																																																																										
Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr																																																																											
100	105		110	Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr		115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																								
	110																																																																										
Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr																																																																											
115	120		125	Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro		130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																														
	125																																																																										
Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro																																																																											
130	135		140	Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu		145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																																				
	140																																																																										
Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu																																																																											
145	150		155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																																										
	155		160	Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr		165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																																												
	160																																																																										
Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr																																																																											
165	170		175	Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val		180	185		190																																																																		
	175																																																																										
Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val																																																																											
180	185		190																																																																								
	190																																																																										

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
 195 200 205
 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
 210 215 220
 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
 225 230 235 240
 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
 245 250 255
 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
 260 265 270
 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
 275 280 285
 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn
 290 295 300
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly
 305 310 315 320
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr
 325 330 335
 Ile Pro Pro Pro Thr
 340 345 350
 Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser
 355 360 365
 Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val
 370 375 380
 Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala
 385 390 395 400
 Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp
 405 410 415
 Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn
 420 425 430
 Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
 435 440

<210> 3
 <211> 1935
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> 2..1272

<400> 3

g gcg gcg cct cca ggg ctc cgg ctc cgg ctc ctg ctg ttg ctc ctt	46
Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu	
1 5 10 15	
tcg gcc gcg gca ctg atc ccc aca ggt gat gga cag aat ctg ttt act	94
Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr	

	20	25	30	
aaa gac gtg aca gtg att gaa gga gaa gtg gca acc atc agc tgc cag Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln	35	40	45	142
gtc aat aag agt gac gac tca gtg atc cag ctc ctg aac ccc aac agg Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn Arg	50	55	60	190
cag acc att tac ttc agg gac ttc agg cct ttg aag gac agc agg ttt Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg Phe	65	70	75	238
cag ctg ctg aat ttt tct agc agt gaa ctc aaa gtg tca ctg acg aat Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr Asn	80	85	90	286
gtc tca atc tcg gat gaa ggg aga tac ttc tgc cag ctc tac acg gac Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr Asp	100	105	110	334
ccc cca cag gag agt tac acc acc atc aca gtc ctg gtt cct cca cgt Pro Pro Gln Glu Ser Tyr Thr Ile Thr Val Leu Val Pro Pro Arg	115	120	125	382
aac ttg atg atc gat atc cag aaa gac acg gca gtt gaa ggg gag gag Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Glu	130	135	140	430
att gaa gtc aac tgt act gcc atg gcc agc aag cca gcg acg acc atc Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile	145	150	155	478
agg tgg ttc aaa ggg aac aag gaa ctc aaa ggc aaa tca gag gtg gag Arg Trp Phe Lys Asn Lys Glu Leu Lys Gly Lys Ser Glu Val Glu	160	165	170	526
gag tgg tcg gac atg tac act gtg acc agt cag ctg atg ctg aag gtg Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val	180	185	190	574
cac aag gag gac gac ggg gtc ccg gtg atc tgc cag gtg gag cac cct His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro	195	200	205	622
gcg gtc act gga aac ctg cag acc cag cgc tat cta gaa gtg cag tat Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr	210	215	220	670
aaa ccg caa gtg cat atc cag atg act tac cct ctg caa ggc cta acc Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr	225	230	235	718
cgg gaa ggg gat gca ttt gag tta acg tgt gaa gcc atc ggg aag ccc Arg Glu Gly Asp Ala Phe Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro	240	245	250	766
cag cct gtg atg gta act tgg gtg aga gtc gat gat gaa atg cct caa Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln	260	265	270	814
cat gcc gta ctg tct ggg cca aac ctg ttc atc aat aac cta aac aaa His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys	275	280	285	862
aca gat aac ggt act tac cgc tgt gag gct tcc aac ata gtg gga aag				910

Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn	Ile	Val	Gly	Lys	
290							295					300				
gct cat tcg gac tat atg ctg tat gta tac gat ccc ccc aca act atc 958																
Ala	His	Ser	Asp	Tyr	Met	Leu	Tyr	Val	Tyr	Asp	Pro	Pro	Thr	Thr	Ile	
305						310					315					
cct cct ccc aca aca acc acc acc act acc acc acc acc acc acc acc 1006																
Pro	Pro	Pro	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	
320						325				330				335		
atc ctt acc atc atc aca gat tct cga gca ggt gaa gag ggg acc att 1054																
Ile	Leu	Thr	Ile	Ile	Thr	Asp	Ser	Arg	Ala	Gly	Glu	Glu	Gly	Thr	Ile	
						340			345				350			
ggg gca gtg gac cac gca gtg att ggt ggc gtc gta gcc gtg gtg gtg 1102																
Gly	Ala	Val	Asp	His	Ala	Val	Ile	Gly	Gly	Val	Val	Ala	Val	Val	Val	
						355			360				365			
ttt gcc atg cta tgc ttg ctc atc att ctg ggc cgc tat ttt gcc aga 1150																
Phe	Ala	Met	Leu	Cys	Leu	Leu	Ile	Ile	Leu	Gly	Arg	Tyr	Phe	Ala	Arg	
						370			375				380			
cat aaa ggt aca tac ttc act cat gaa gcc aaa gga gcc gat gac gca 1198																
His	Lys	Gly	Thr	Tyr	Phe	Thr	His	Glu	Ala	Lys	Gly	Ala	Asp	Asp	Ala	
						385			390				395			
gca gac gca gac aca gct ata atc aat gca gaa gga gga cag aac aac 1246																
Ala	Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu	Gly	Gly	Gln	Asn	Asn	
						400			405				410			415
tcc gaa gaa aag aaa gag tac ttc at ctagatcagc ctttttgttc 1292																
Ser	Glu	Glu	Lys	Lys	Glu	Tyr	Phe									
						420										
caatgaggtg tccaaactggc ctgttttagat gataaagaga cagtatact ggaactttcg 1352																
agaagctcgt	gtggttttt	gtttttttt	gttttttat	gagtgggtgg	agagatgcga											1412
gactggaaag	gcttggatt	tgcaatgtac	aaacaaaaac	aaagaatgtt	ctttgaaaagt											1472
acactctgct	gtttgacacc	tcttttaat	ctggttttaa	tttgctttgg	gttttgggtt											1532
tttttggttt	tttggttttt	tcatttat	ttcttcctac	caagtcaaac	ttgggtactt											1592
ggatttggtt	tcggtagatt	gcagaaaatt	ctgtgccttg	ttttcattc	gtttgttgc											1652
tttctccct	cttgcccatt	tatTTTCCC	aaaatcaaat	ttgtttttt	ccccctccca											1712
aacctccat	ttttggaaat	tgacctgctg	gaattcctaa	gactttctcc	ctgttgcag											1772
tttctttat	ttgtgttaac	ggtgactgct	ttctgttcca	aattcagttt	cataaaagga											1832
aaaccagcac	aatttagatt	tcatagttca	gaatttagtg	tctccatgtat	gcatccttct											1892
ctgttgtgt	aaagatttgg	gtgaagaaaa	aaaaaaaaaa	aaa												1935

<210> 4
<211> 423
<212> PRT
<213> Mus musculus

<400> 4

Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Ser

1	5	10	15
Ala Ala Ala Leu Ile Pro Thr Gly Asp	Gly Gln Asn Leu Phe Thr Lys		
20	25	30	
Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln Val			
35	40	45	
Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn Arg Gln			
50	55	60	
Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg Phe Gln			
65	70	75	80
Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr Asn Val			
85	90	95	
Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr Asp Pro			
100	105	110	
Pro Gln Glu Ser Tyr Thr Ile Thr Val Leu Val Pro Pro Arg Asn			
115	120	125	
Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Glu Ile			
130	135	140	
Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg			
145	150	155	160
Trp Phe Lys Gly Asn Lys Glu Leu Lys Gly Lys Ser Glu Val Glu Glu			
165	170	175	
Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His			
180	185	190	
Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala			
195	200	205	
Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys			
210	215	220	
Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr Arg			
225	230	235	240
Glu Gly Asp Ala Phe Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro Gln			
245	250	255	
Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln His			
260	265	270	
Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys Thr			
275	280	285	
Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys Ala			
290	295	300	
His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile Pro			
305	310	315	320
Pro Pro Thr Ile			
325	330	335	
Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Ile Gly			
340	345	350	
Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val Val Phe			
355	360	365	

Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg His
370 375 380

Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala
385 390 395 400

Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser
405 410 415

Glu Glu Lys Lys Glu Tyr Phe
420

<210> 5
<211> 29
<212> Oligonucleotide
<213> Homo sapien

<400> 5

tatgtcgaca tggcgagtgt agtgctgcc 29

<210> 6
<211> 30
<212> Oligonucleotide
<213> Homo sapien

<400> 6

atatacatct atgatccact gccctgatcg 30

<210> 7
<211> 1820
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> 157..1452

<400> 7

aagcttggca cgaggcggtc cccacctcg 60

ctttcggtca acatcgtagt ccaccccctc cccatcccc 120

gccagcgccc agccagggag ccggccggga agcgcg atg ggg gcc cca gca 174
Met Gly Ala Pro Ala Ala
1 5

tcg ctc ctg ctc ctg ctc ctg ttc gcc tgc tgc tgg gcg ccc ggc 222
Ser Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly
10 15 20

ggg gcc aac ctc tcc cag gac ggc tac tgg cag gag cag gat ttg gag 270
Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp Gln Glu Gln Asp Leu Glu
25 30 35

ctg gga act ctg gct cca ctc gac gag gcc atc agc tcc aca gtc tgg 318
Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala Ile Ser Ser Thr Val Trp
40 45 50

agc agc cct gac atg ctg gcc agt caa gac agc cag ccc tgg aca tct 366
Ser Ser Pro Asp Met Leu Ala Ser Gln Asp Ser Gln Pro Trp Thr Ser

55	60	65	70	
gat gaa aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val 75 80 85				414
aaa gat cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln 90 95 100				462
act ctc tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln 105 110 115				510
ctg gtt acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser Ile Ser Asn Val 120 125 130				558
gcc ctg gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro 135 140 145 150				606
gtg cga act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys 155 160 165				654
ccc atc atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala 170 175 180				702
acc cta aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr 185 190 195				750
tgg aga aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln 200 205 210				798
gaa gat ccc aat ggt aaa acc ttc act gtc agc agc tcg gtg aca ttc Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Val Thr Phe 215 220 225 230				846
cag gtt acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn 235 240 245				894
cat gaa tct cta aag gga gct gac aga tcc acc tct caa cgc att gaa His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu 250 255 260				942
gtt tta tac aca cca act gcg atg att agg cca gac cct ccc cat cct Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro 265 270 275				990
cgt gag ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca Arg Glu Gly Gln Lys Leu Leu His Cys Glu Gly Arg Gly Asn Pro 280 285 290				1038
gtc ccc cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu 295 300 305 310				1086
aag atg acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser 315 320 325				1134
gac agt ggc acc tac ggc tgc aca gcc acc agc aac atg ggc agc tac				1182

Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr
 330 335 340
 aag gcc tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc 1230
 Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser
 345 350 355
 tcc tcc agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att 1278
 Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile
 360 365 370
 gtc ttc ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc 1326
 Val Phe Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile
 375 380 385 390
 cg^g cac aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat 1374
 Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp
 395 400 405
 gct cca gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca 1422
 Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Ser
 410 415 420
 gga ggg gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc 1472
 Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 425 430
 ctgcgc^{cccccc} cagggccct gtggggactg ctggggccgt caccaacccg gacttgtaca 1532
 gagcaaccgc agggccgccc ctcccgcttg ctccccagcc cacccacccc cctgtacaga 1592
 atgtctgctt tgggtgcgg^t tttgtactcg gtttggaaatg gggagggagg agggcggggg 1652
 gaggggaggg ttgccctcag cccttccgt ggcttctctg catttgggtt attattattt 1712
 ttgttaacaat cccaaatcaa atctgtctcc aggctggaga ggcaggagcc ctggggtgag 1772
 aaaagcaaaa aacaaacaaa aaaaaaaaaa aaaaattcct gcggccgc 1820

 <210> 8
 <211> 432
 <212> PRT
 <213> Homo sapien

 <400> 8

 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp
 20 25 30
 Gln Glu Gln Asp Leu Glu Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala
 35 40 45
 Ile Ser Ser Thr Val Trp Ser Ser Pro Asp Met Leu Ala Ser Gln Asp
 50 55 60
 Ser Gln Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val
 65 70 75 80
 Val Leu Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp
 85 90 95
 Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu
 100 105 110

Arg Asp Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser
 115 120 125
 Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys
 130 135 140
 Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val
 145 150 155 160
 Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu
 165 170 175
 Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys
 180 185 190
 Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly
 195 200 205
 Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val
 210 215 220
 Ser Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser
 225 230 235 240
 Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser
 245 250 255
 Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg
 260 265 270
 Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu His Cys
 275 280 285
 Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu
 290 295 300
 Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe
 305 310 315 320
 Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr
 325 330 335
 Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp
 340 345 350
 Pro Ser Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly
 355 360 365
 Gly Ile Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe
 370 375 380
 Leu Gly His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu
 385 390 395 400
 Ala Lys Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn
 405 410 415
 Ala Glu Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 420 425 430

<210> 9
 <211> 1718
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> 157..1350
 <400> 9

aagcttggca	cgaggcggtc	cccacctcg	ccccgggctc	cgaagcggct	cggggggcgcc	60
ctttcggtca	acatcgtagt	ccaccccctc	cccatccccca	ccccccgggg	attcaggctc	120
gccagcgccc	agccagggag	ccggccggga	agcgcg	atg ggg gcc cca	gcc	174
				Met Gly Ala Pro	Ala Ala	
				1	5	
tcg ctc ctg	ctc ctg ctg	ttc tgc	tgc tgg	gct ccc	ggc	222
Ser Leu Leu	Leu Leu Leu	Leu Phe	Ala Cys	Cys Trp	Ala Pro	Gly
10	15	15	20			
ggg gcc aac	ctc tcc cag	gac gac	agc cag	ccc tgg	aca tct	270
Gly Ala Asn	Leu Ser Gln	Asp Asp	Ser Gln	Pro Trp	Thr Ser Asp	Glu
25	30	30	35			
aca gtg gtg	gct ggt ggc	acc gtg gtg	ctc aag tgc	caa gtg aaa	aat gat	318
Thr Val Val	Ala Gly Gly	Thr Val Val	Leu Lys	Cys Gln	Val Lys Asp	
40	45	45	50			
cac gag gac	tca tcc ctg	caa tgg tct	aac cct gct	cag cag act	ctc	366
His Glu Asp	Ser Ser Leu	Gln Trp	Ser Asn	Pro Ala Gln	Gln Thr Leu	
55	60	60	65	70		
tac ttt ggg	gag aag aga	gcc ctt cga	gat aat cga	att cag ctg	gtt	414
Tyr Phe Gly	Glu Lys Arg	Ala Leu Arg	Asp Asn Arg	Ile Gln	Leu Val	
75	80	80	85			
acc tct acg	ccc cac gag	ctc agc atc	agc atc agc	aat gtg gcc	ctg	462
Thr Ser Thr	Pro His Glu	Leu Ser Ile	Ser Ile Ser	Asn Val Ala	Leu	
90	95	95	100			
gca gac gag	ggc gag tac	acc tgc tca	atc atc tt	act atg cct	gtg cga	510
Ala Asp Glu	Gly Glu Tyr	Thr Cys Ser	Ile Phe Thr	Met Pro Val	Arg	
105	110	110	115			
act gcc aag	tcc ctc gtc	act gtg cta	gga att cca	cag aag ccc	atc	558
Thr Ala Lys	Ser Leu Val	Thr Val Leu	Gly Ile	Pro Gln Lys	Pro Ile	
120	125	125	130			
atc act ggt	tat aaa tct	tca tta cgg	gaa aaa gac	aca gcc acc	cta	606
Ile Thr Gly	Tyr Lys Ser	Ser Leu Arg	Glu Lys Asp	Thr Ala Thr	Leu	
135	140	140	145	150		
aac tgt cag	tct tgg agc	aag cct gca	gcc cg	ctc acc tgg	aga	654
Asn Cys Gln	Ser Ser Gly	Lys Pro Ala	Ala Arg	Leu Thr Trp	Arg	
155	160	160	165			
aag ggt gac	caa gaa ctc	cac gga	caa acc cgc	ata cag gaa	gat	702
Lys Gly Asp	Gln Glu Leu	His Gly	Glu Pro	Thr Arg Ile	Gln Glu Asp	
170	175	175	180			
ccc aat ggt	aaa acc ttc	act gtc	agc agc tcg	gtg aca ttc	cag gtt	750
Pro Asn Gly	Lys Thr Phe	Thr Val	Ser Ser	Ser Val	Thr Phe Gln	Val
185	190	190	195			
acc cgg gag	gat gat ggg	gct agc atc	gtg tgc	tct gtg aac	cat gaa	798
Thr Arg Glu	Asp Asp Gly	Ala Ser Ile	Val Cys Ser	Val Asn His	Glu	
200	205	205	210			
tct cta aag	gga gct gac	aga tcc acc	tct caa	cgc att gaa	gtt tta	846

Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser	Gln	Arg	Ile	Glu	Val	Leu		
215				220			225			230							
tac	aca	cca	act	gcg	atg	att	agg	cca	gac	cct	ccc	cat	cct	cgt	gag	894	
Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp	Pro	Pro	His	Pro	Arg	Glu		
				235				240			245						
ggc	cag	aag	ctg	ttg	cta	cac	tgt	gag	ggt	cgc	ggc	aat	cca	gtc	ccc	942	
Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly	Arg	Gly	Asn	Pro	Val	Pro		
				250				255			260						
cag	cag	tac	cta	tgg	gag	aag	gag	ggc	agt	gtg	cca	ccc	ctg	aag	atg	990	
Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser	Val	Pro	Pro	Leu	Lys	Met		
				265				270			275						
acc	cag	gag	agt	gcc	ctg	atc	ttc	cct	ttc	ctc	aac	aag	agt	gac	agt	1038	
Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe	Leu	Asn	Lys	Ser	Asp	Ser		
				280			285			290							
ggc	acc	acc	tac	ggc	tgc	aca	gcc	acc	agc	aac	atg	ggc	agc	tac	aag	gcc	1086
Gly	Thr	Tyr	Gly	Cys	Thr	Ala	Thr	Ser	Asn	Met	Gly	Ser	Tyr	Lys	Ala		
				295			300			305			310				
tac	tac	acc	ctc	aat	gtt	aat	gac	ccc	agt	ccg	gtg	ccc	tcc	tcc	tcc	1134	
Tyr	Tyr	Thr	Leu	Asn	Val	Asn	Asp	Pro	Ser	Pro	Val	Pro	Ser	Ser	Ser		
				315				320			325						
agc	acc	acc	tac	cac	gcc	atc	atc	ggt	ggg	atc	gtg	gct	ttc	att	gtc	ttc	1182
Ser	Thr	Tyr	His	Ala	Ile	Ile	Gly	Gly	Ile	Val	Ala	Phe	Ile	Val	Phe		
				330				335			340						
ctg	ctg	ctc	atc	atg	ctc	atc	ttc	ctt	ggc	cac	tac	ttg	atc	cg	cac	1230	
Leu	Leu	Leu	Ile	Met	Leu	Ile	Phe	Leu	Gly	His	Tyr	Leu	Ile	Arg	His		
				345				350			355						
aaa	gga	acc	tac	ctg	aca	cat	gag	gca	aaa	ggc	tcc	gac	gat	gct	cca	1278	
Lys	Gly	Thr	Tyr	Leu	Thr	His	Glu	Ala	Lys	Gly	Ser	Asp	Asp	Ala	Pro		
				360			365			370							
gac	gcg	gac	acg	gcc	atc	atc	aat	gca	gaa	ggc	ggg	cag	tca	gga	ggg	1326	
Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu	Gly	Gly	Gln	Ser	Gly	Gly		
				375			380			385			390				
gac	gac	aag	aag	gaa	tat	ttc	atc	tagaggcgcc	tgcccacttc	ctgcgcccc						1380	
Asp	Asp	Lys	Lys	Glu	Tyr	Phe	Ile										
				395													
cagggggccct	gtggggactg	ctggggccgt	caccaacccg	gacttgtaca	gagcaaccgc											1440	
agggccgccc	ctcccgcttg	ctccccagcc	cacccacccc	cctgtacaga	atgtctgctt											1500	
tgggtgcgt	tttgtactcg	gtttggaatg	gggagggagg	agggcggggg	gaggggaggg											1560	
ttgccctcag	ccctttccgt	ggcttctctg	catttgggtt	attattattt	ttgttaacaat											1620	
cccaaatacaa	atctgtctcc	aggctggaga	ggcaggagcc	ctggggtgag	aaaagcaaaa											1680	
aacaaacaaaa	aaaaaaaaaa	aaaaattcct	gcggccgc													1718	

<210> 10
 <211> 398
 <212> PRT
 <213> Homo sapien

<400> 10

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285
 Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300
 Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320
 Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335
 Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350
 His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys

355

360

365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
385 390 395